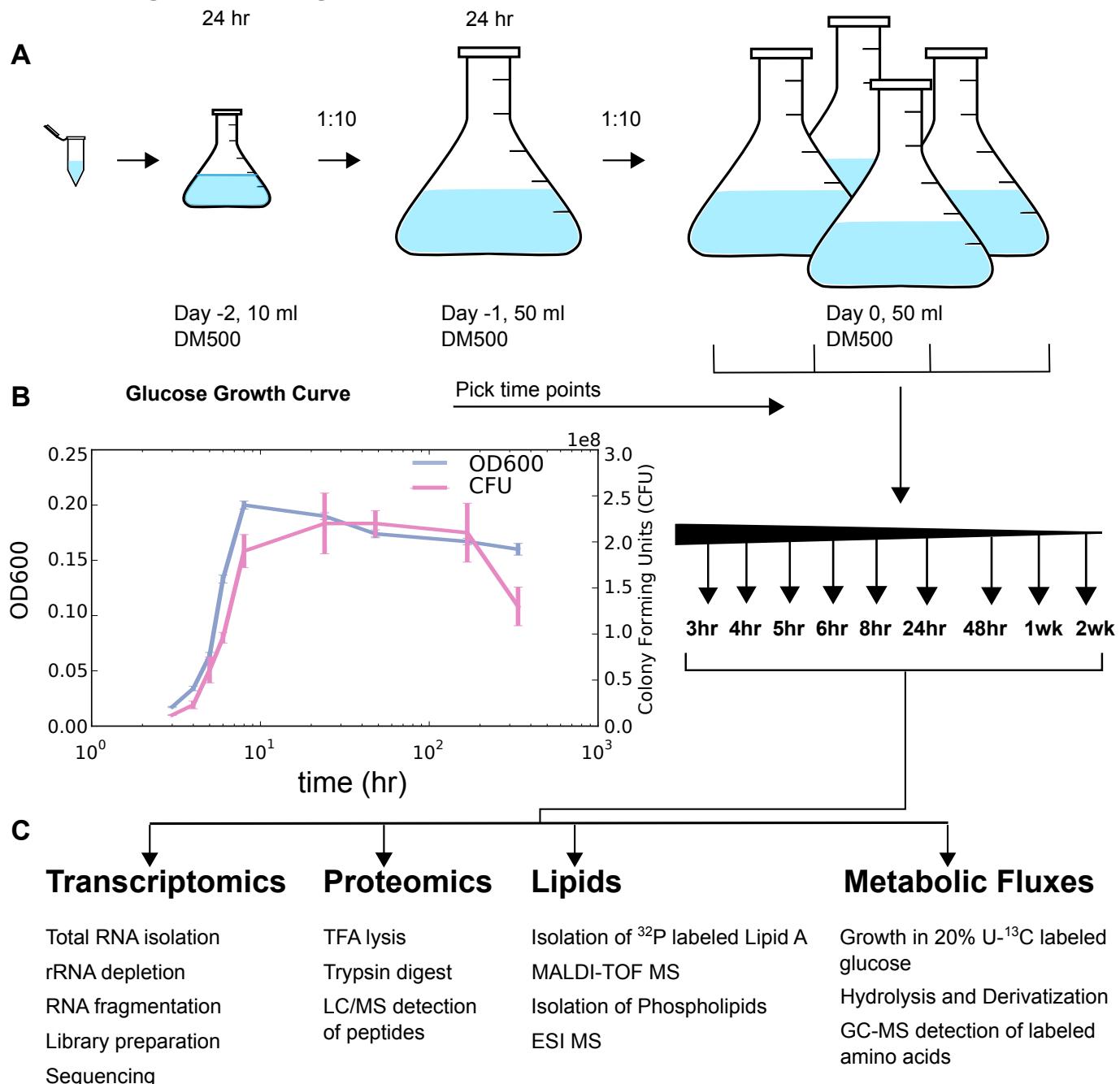
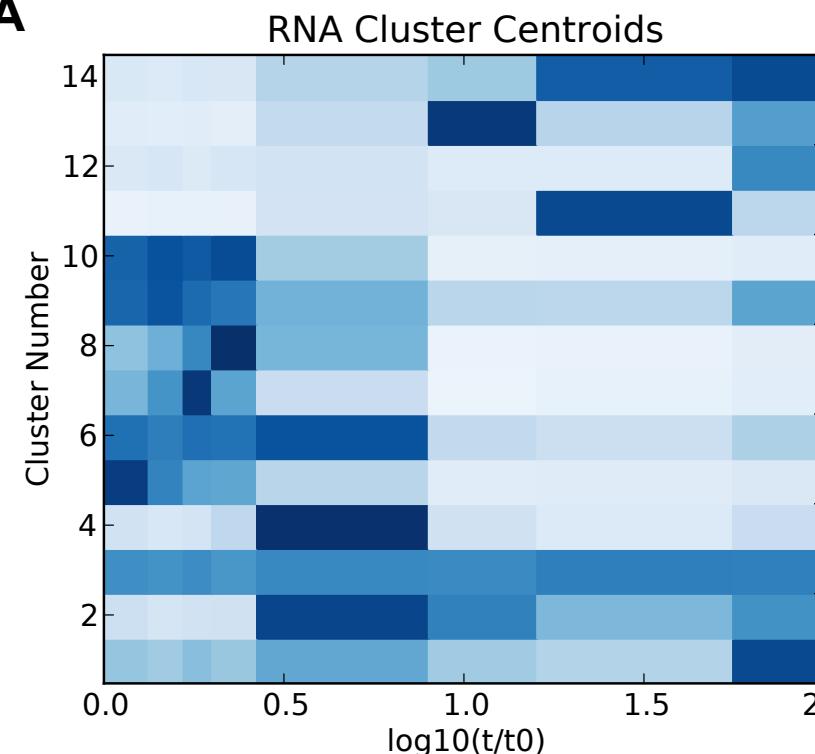
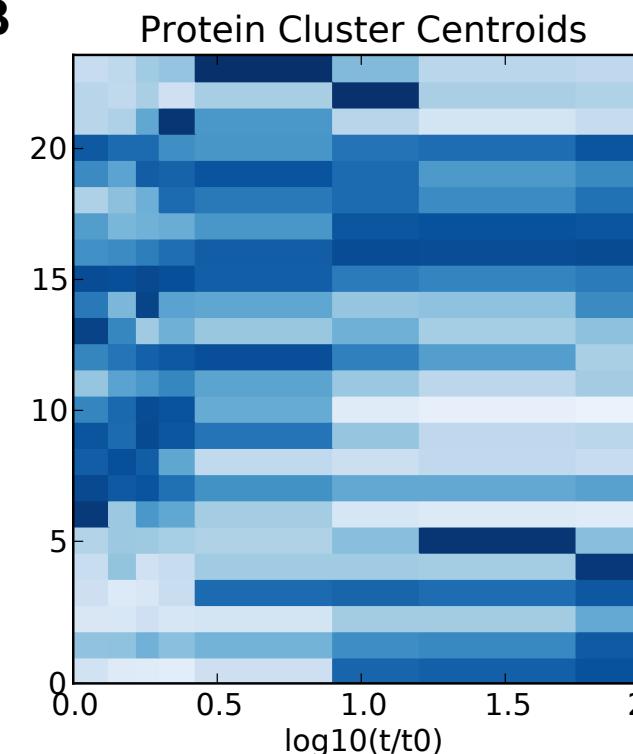
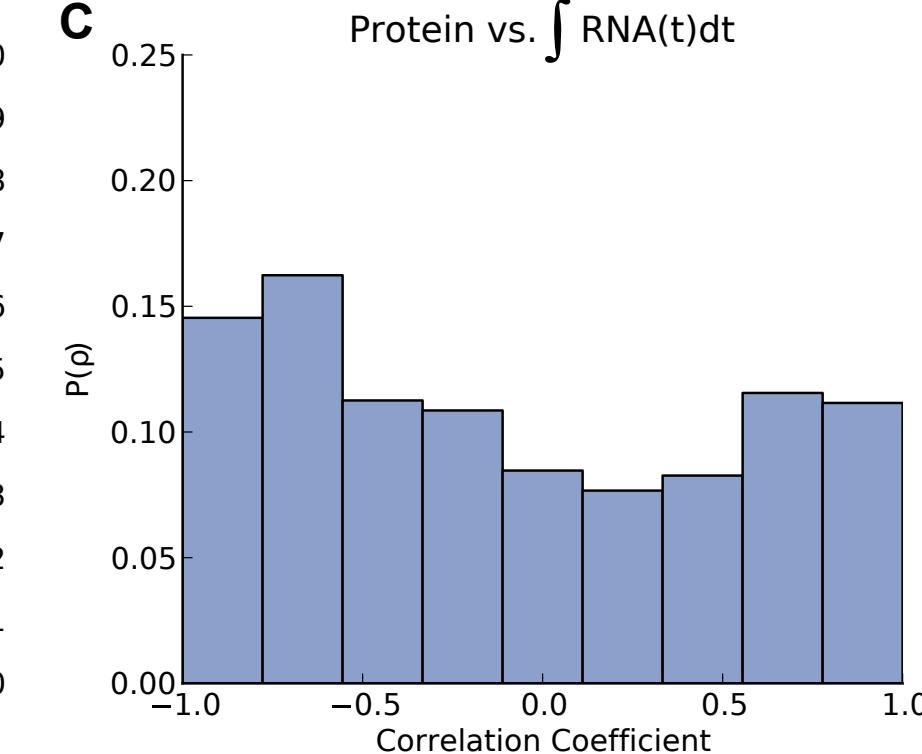
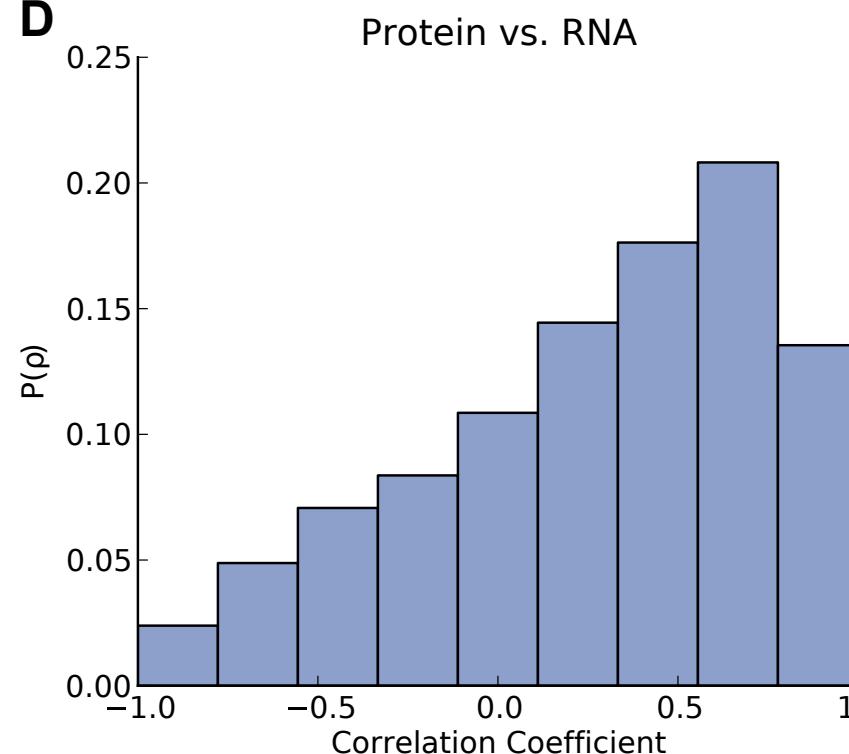
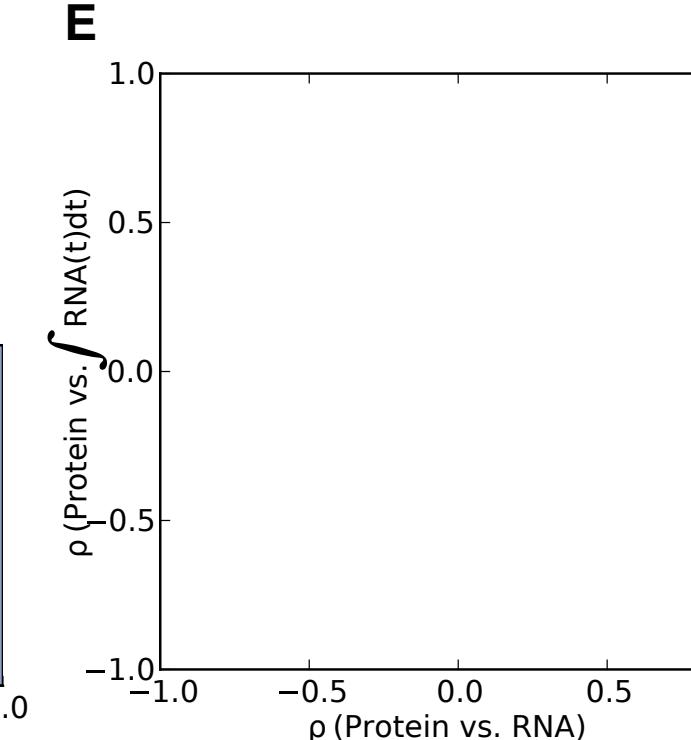
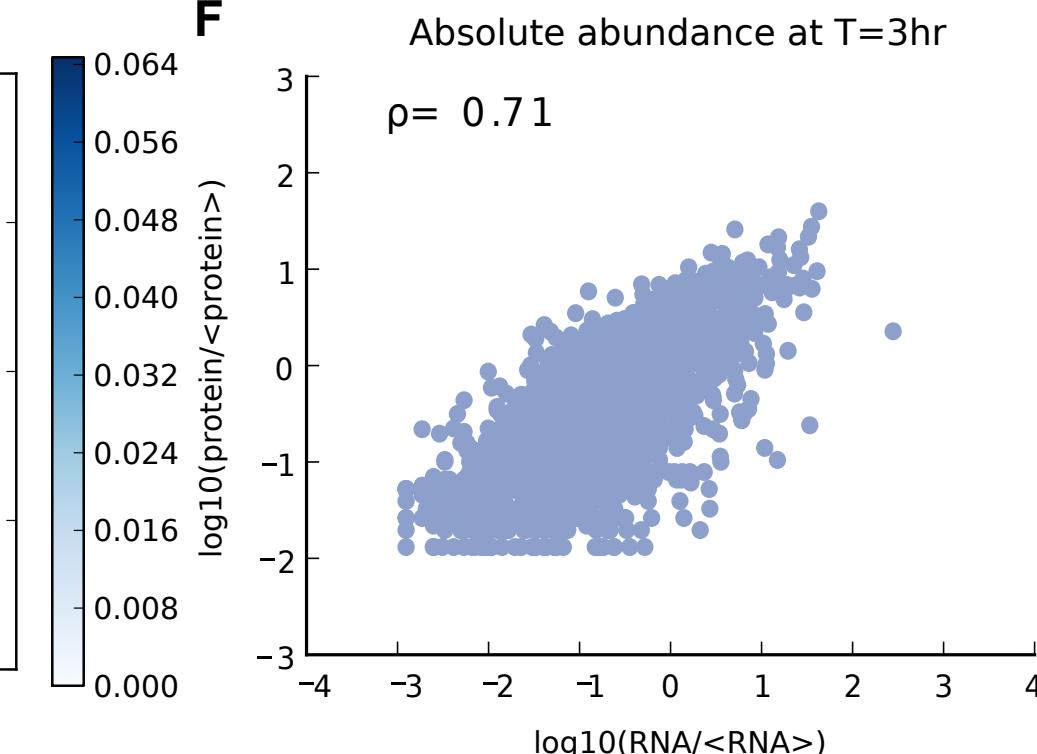


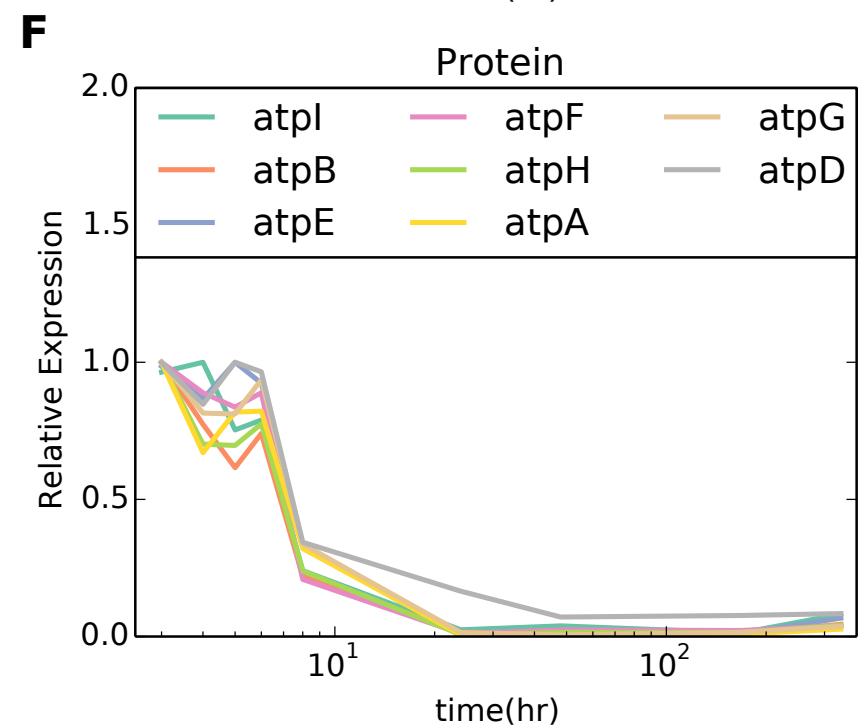
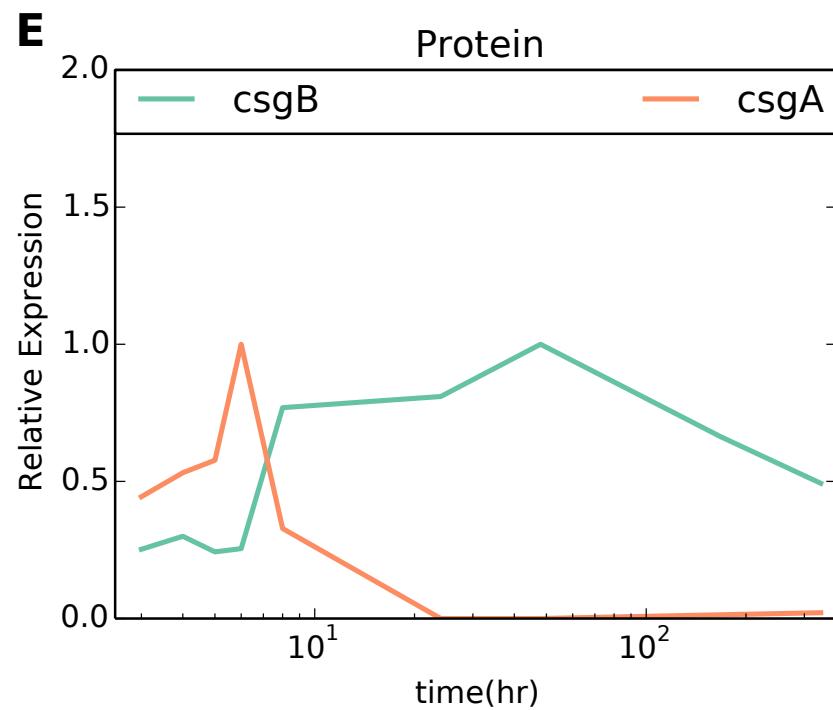
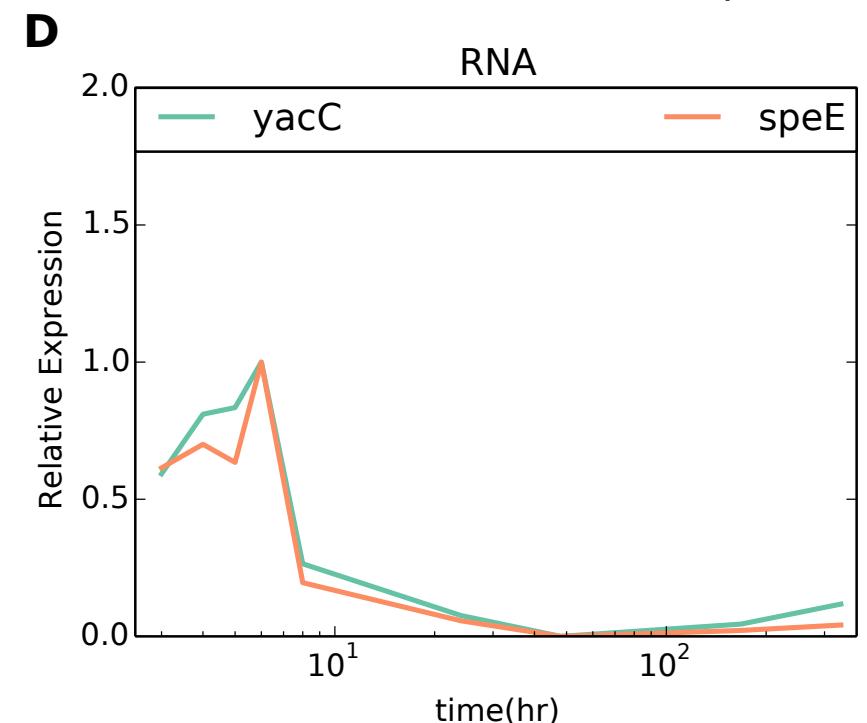
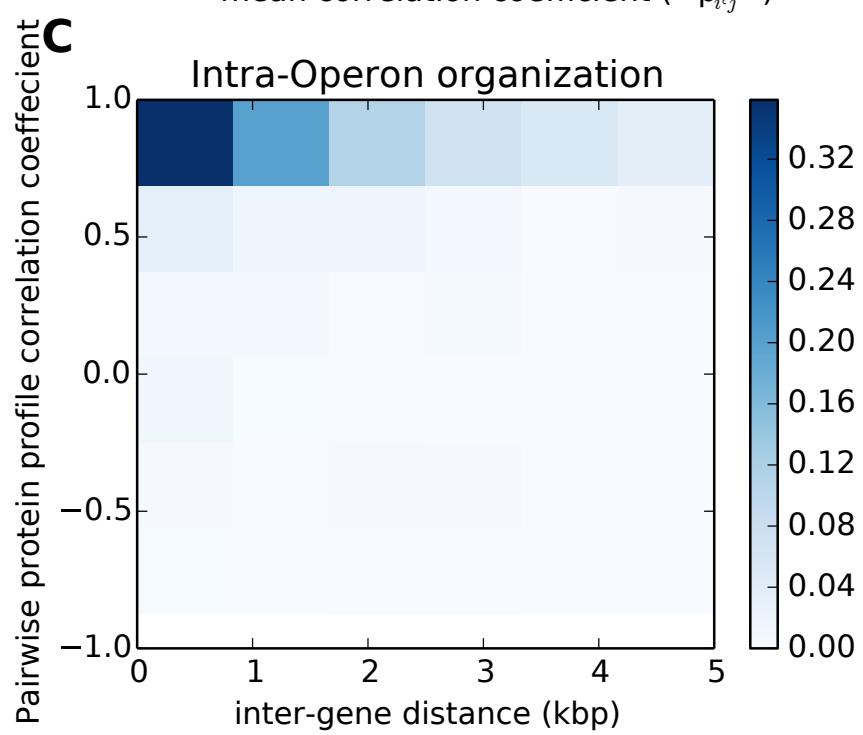
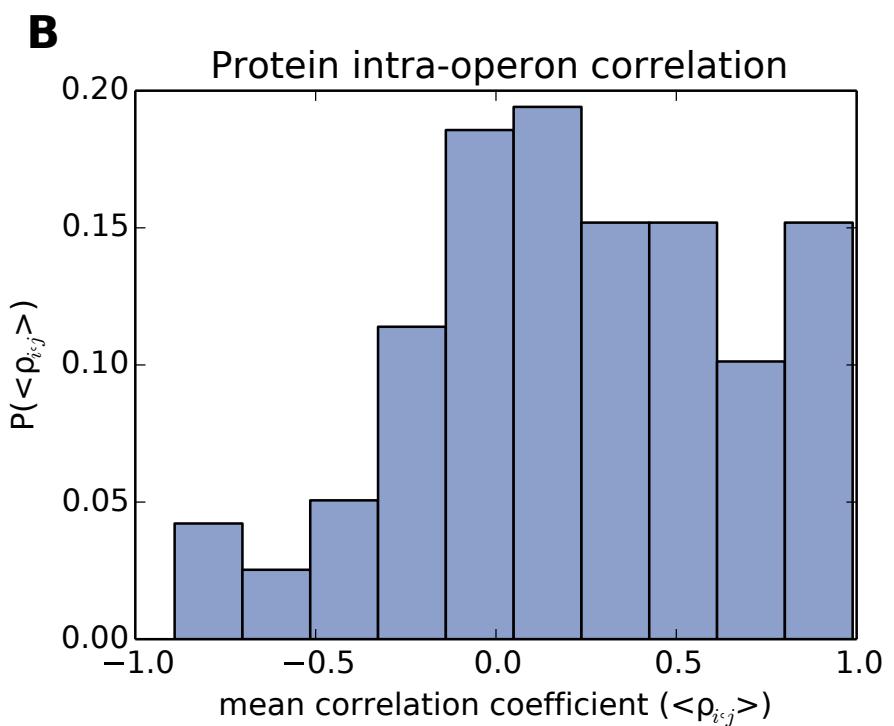
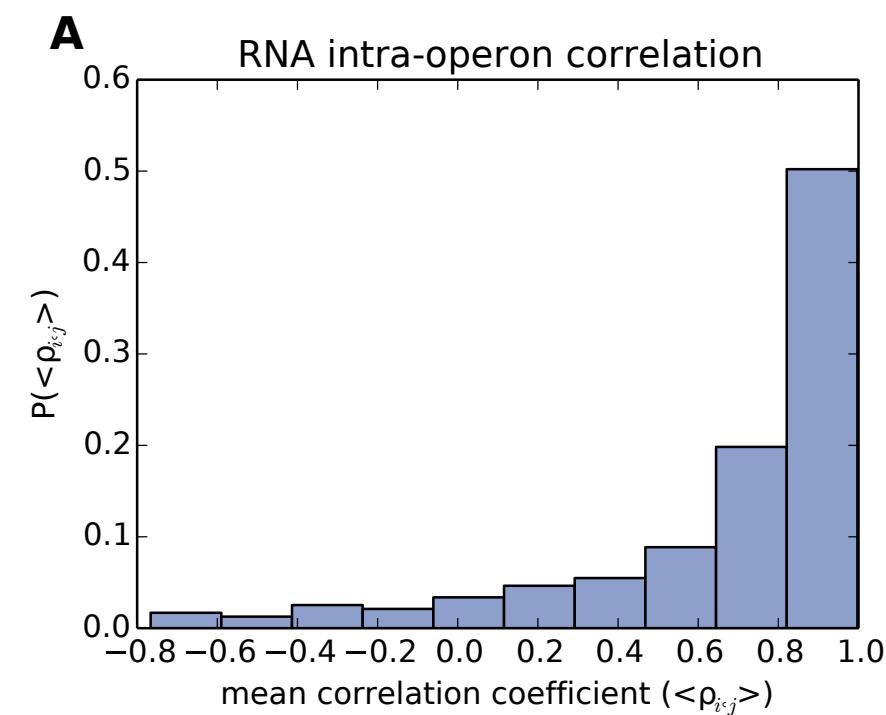
# Figure 1

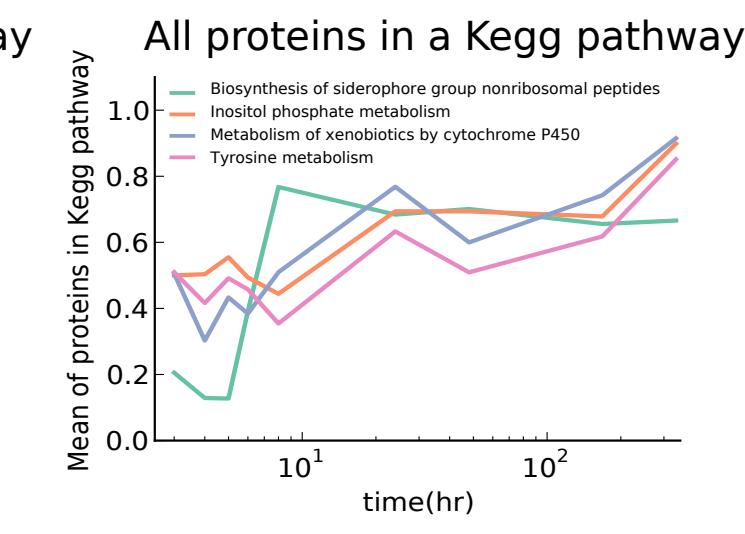
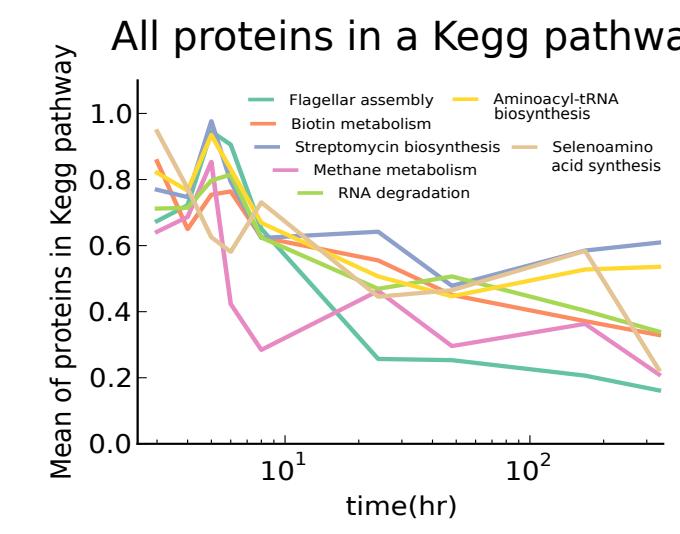
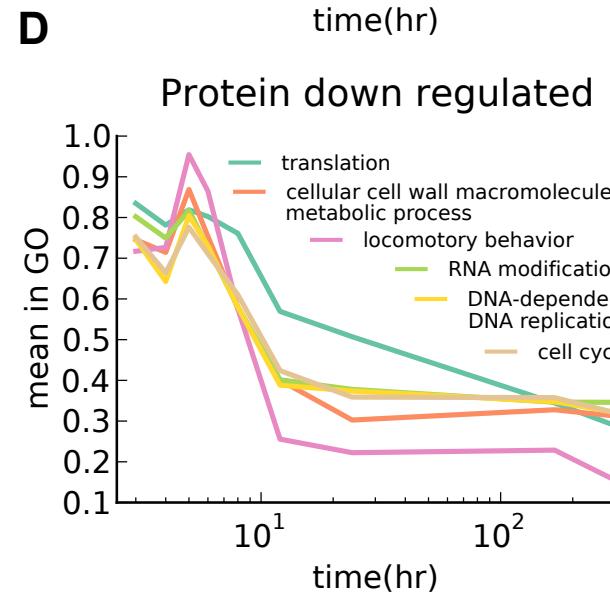
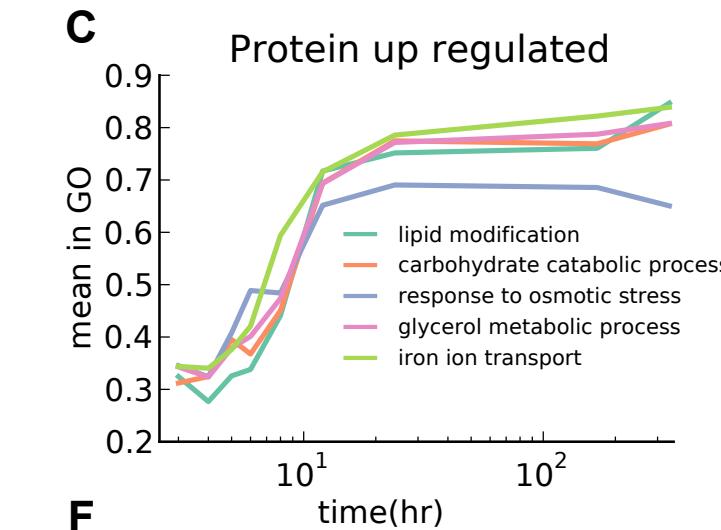
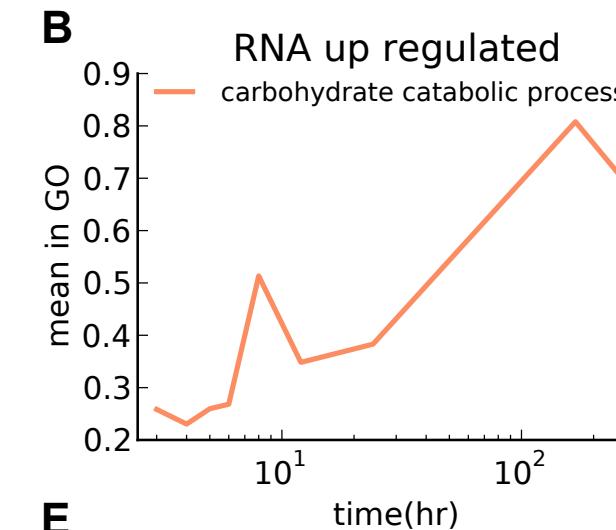
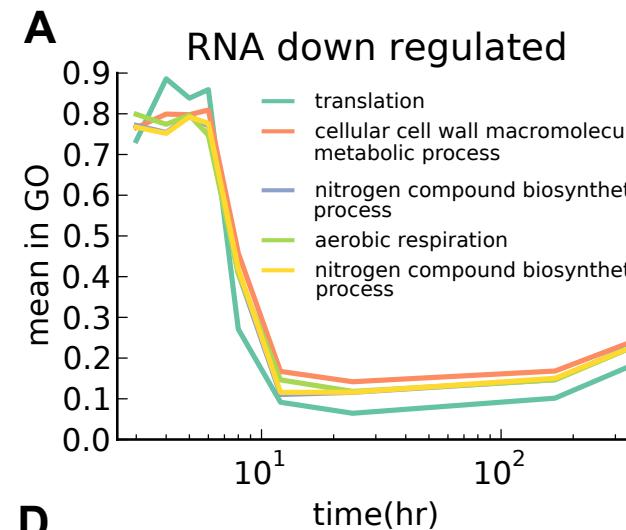
## Glucose growth, long-term starvation, and multiplexed data acquisition



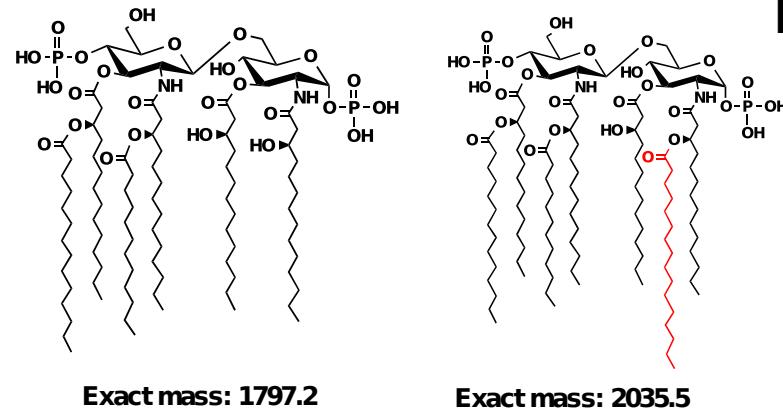
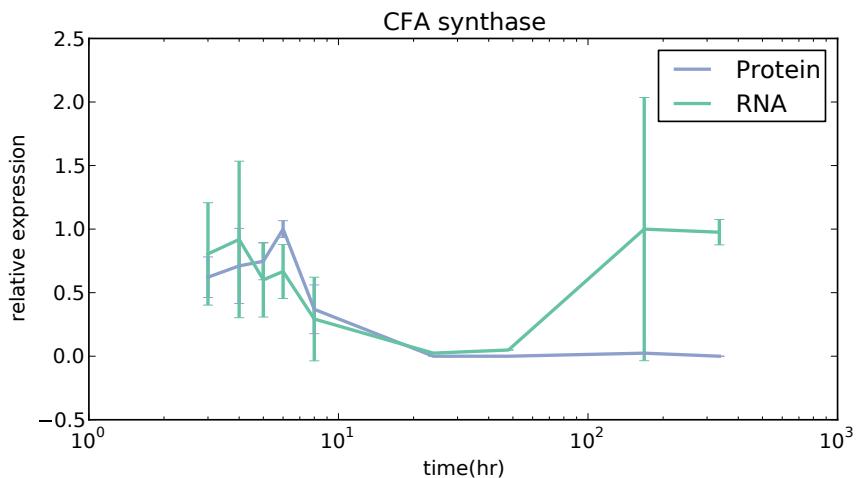
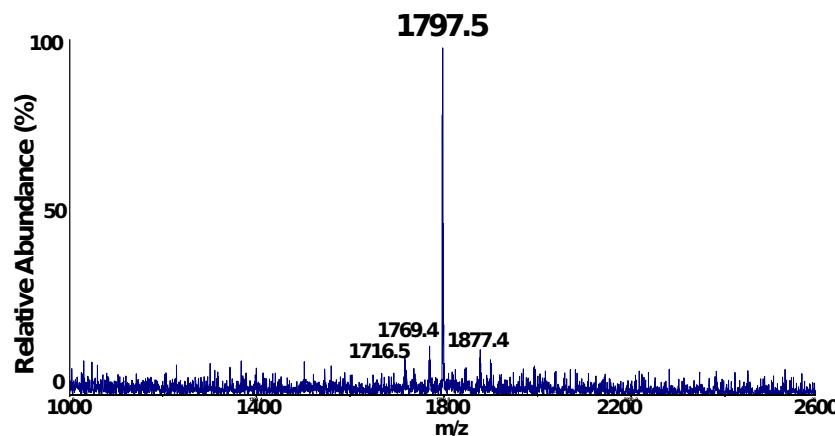
**Figure 2****A****B****C****D****E****F**

## **Figure 3**

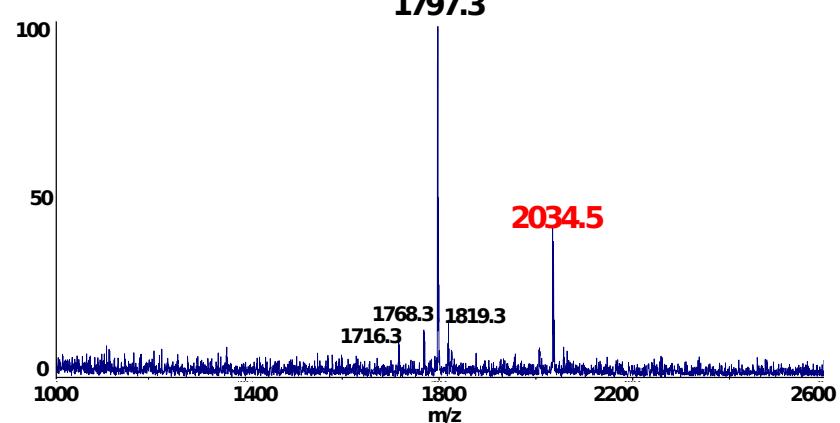
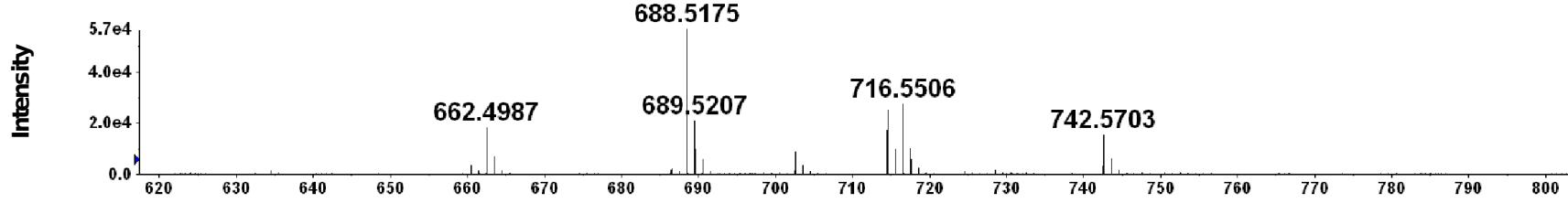
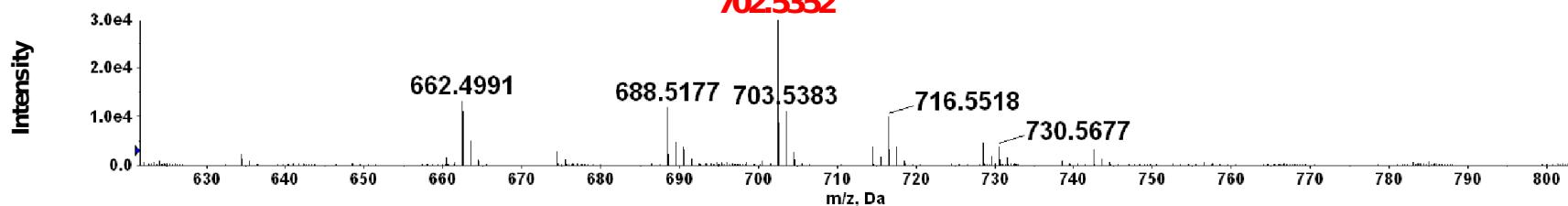


**Figure 4**

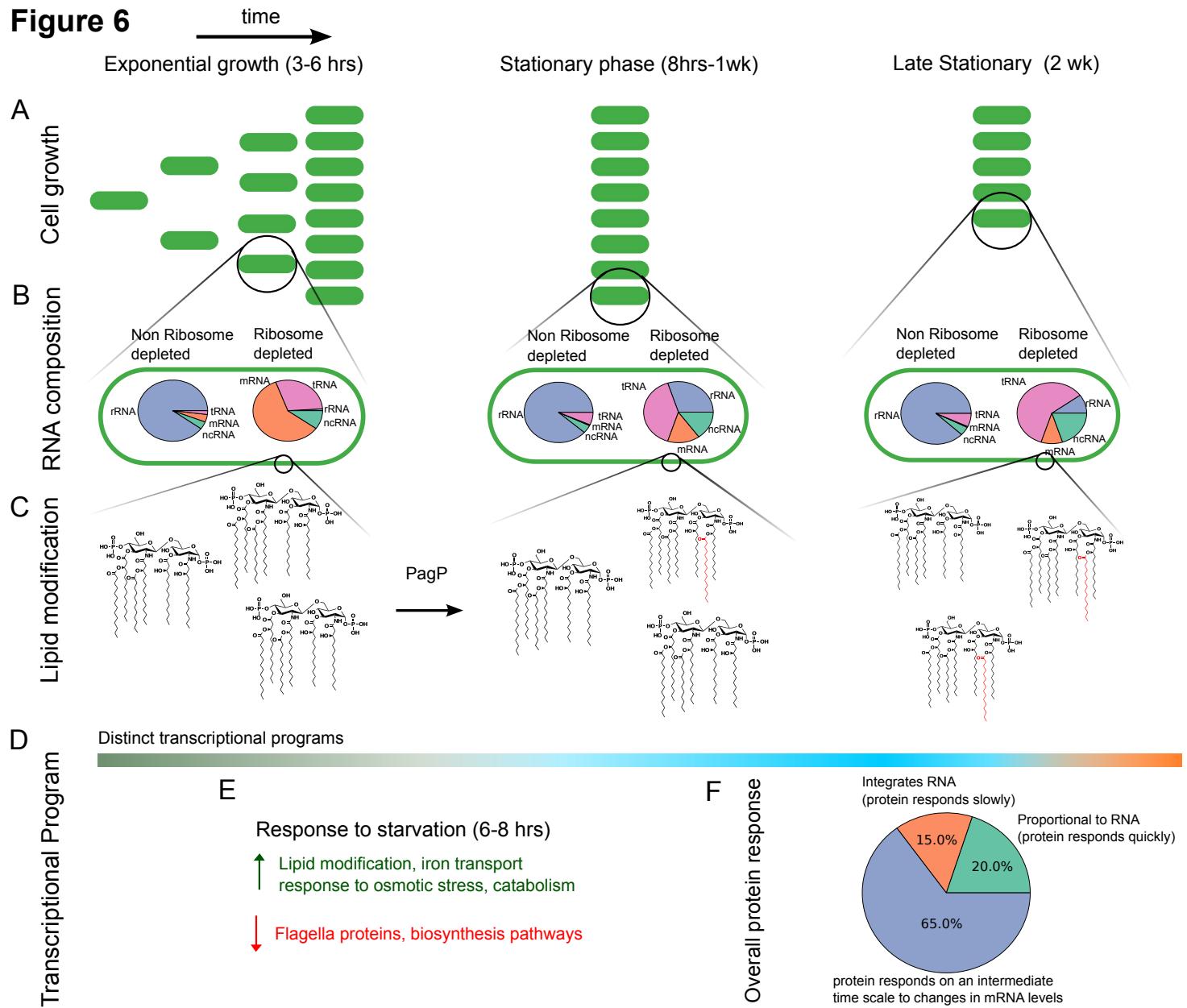
# Figure 5

**A****B****C**

2 weeks

**D 6 hours****2 weeks**

**Figure 6**

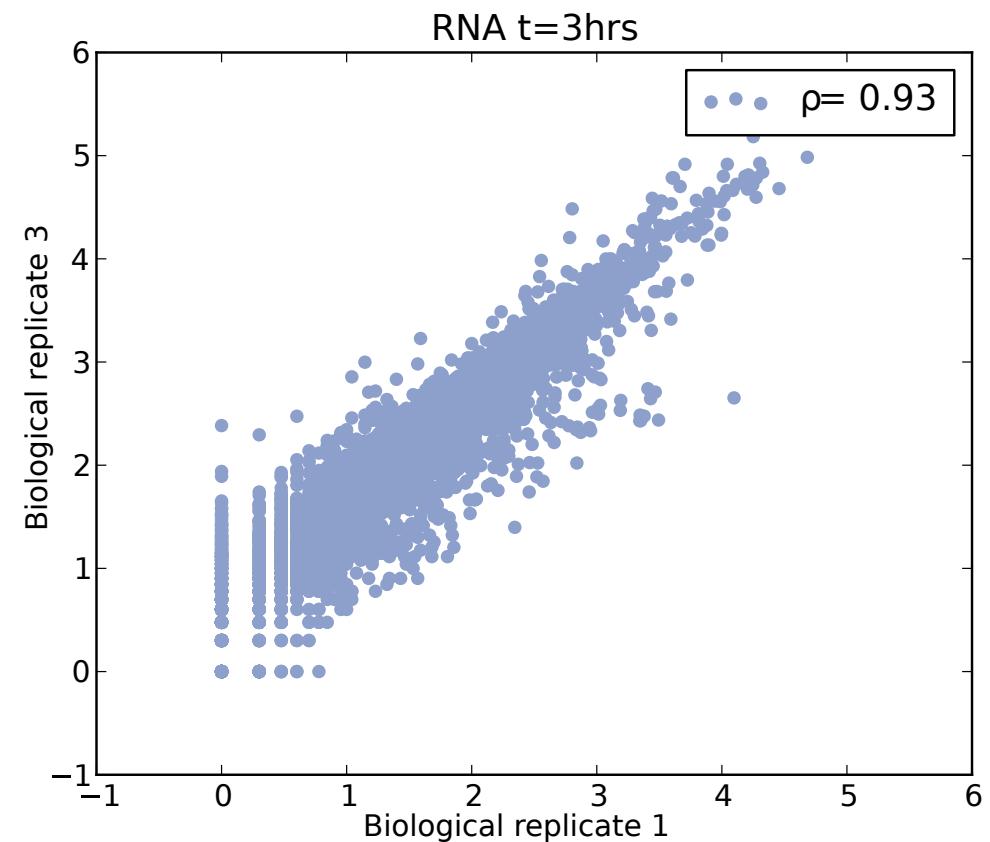
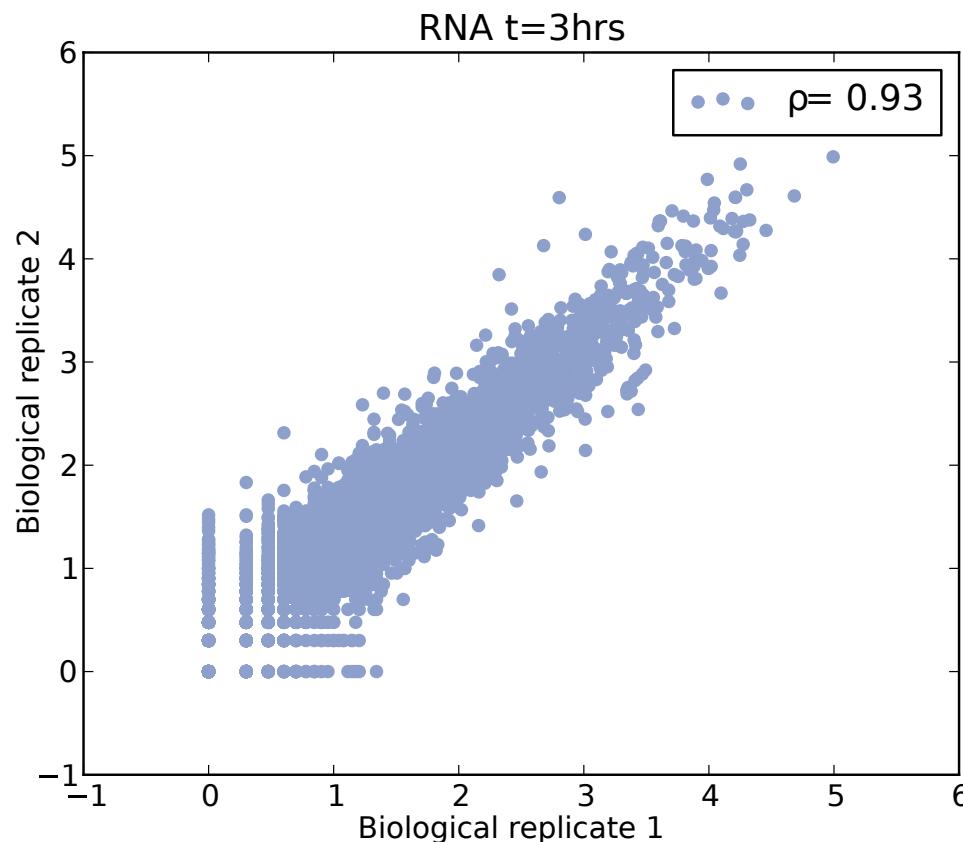
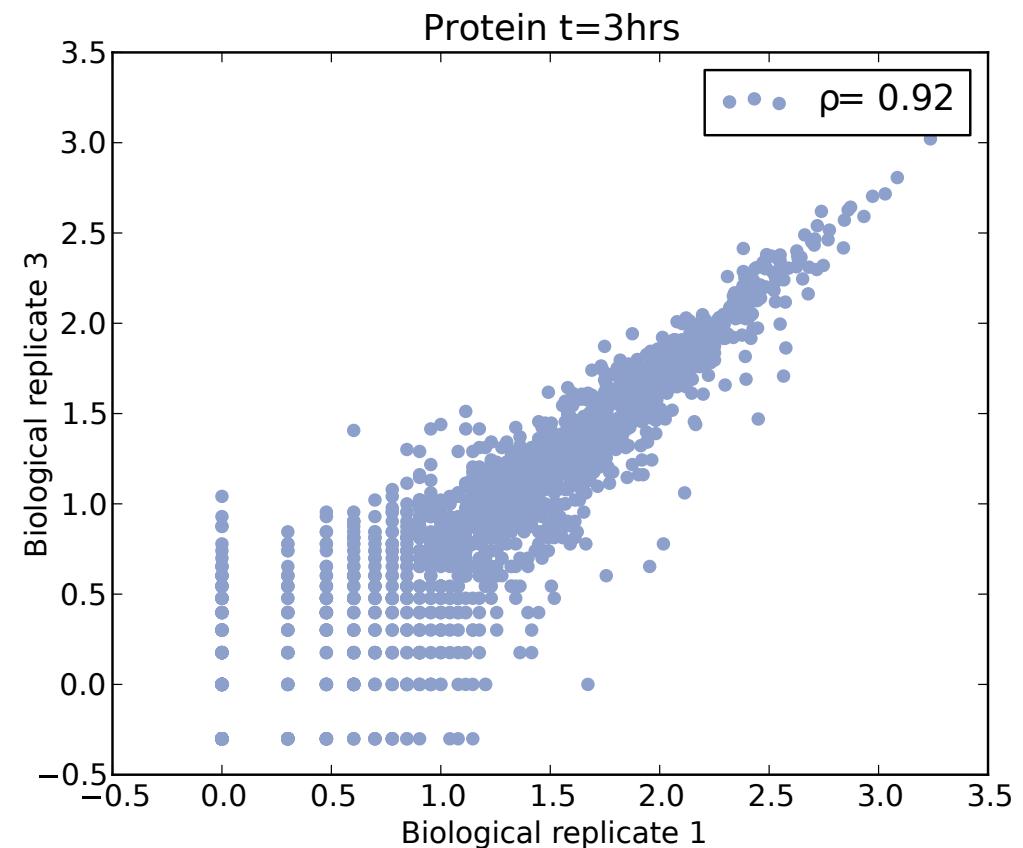
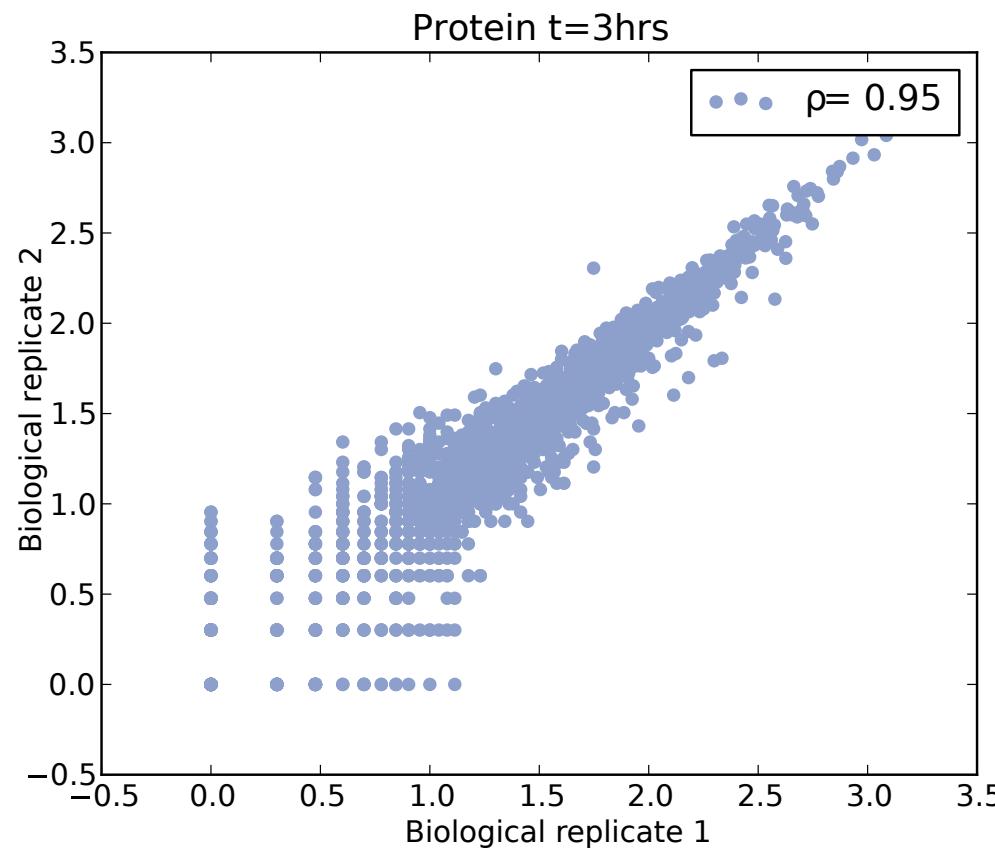


**Table 1**

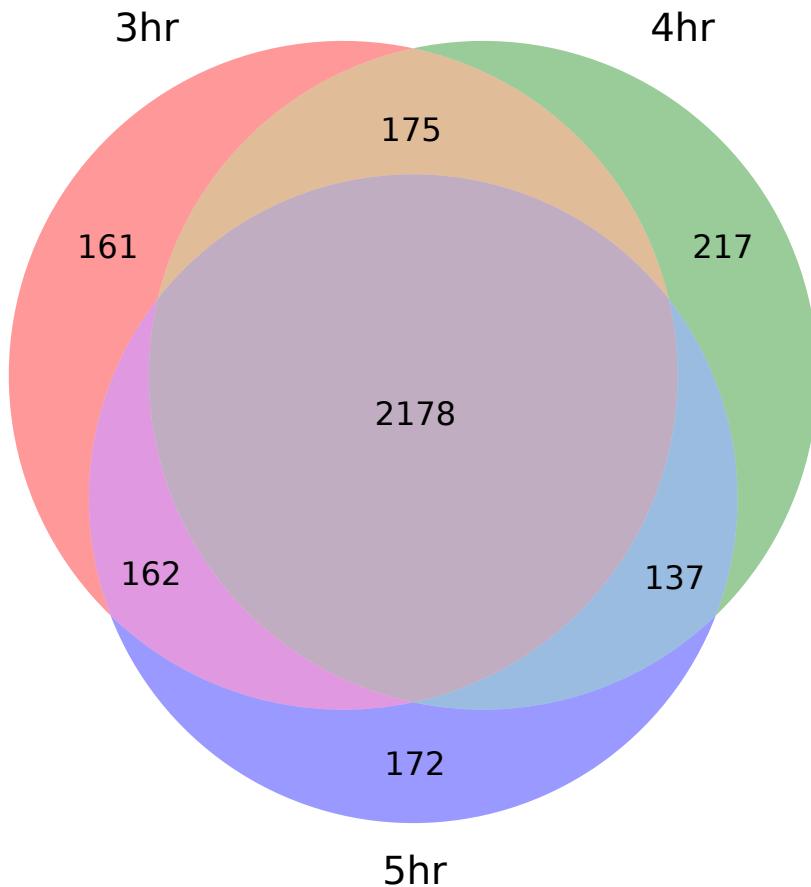
Publication	N proteins found	Cutoff	Method	#RNAs	Cutoff	Method
This study	2648 * (at 3hrs)	FDR<1%	Shotgun MS	4116 genes, 89 sRNA, 85 tRNA (at 3hrs)	Alignment quality>10	RNA-seq
Yoon et al. 2012	60	fold change>2	2-D gel	4144 gene probes (REL606 strain)	NA	Microarray
Taniguchi et al.i 2012	1018	NA	YFP fusion	137	95% confidence	FISH
Lewis et al. 2010	~1,000	P-value<0.05	Shotgun MS			
Lewis et al. 2009				4428 gene probes	NA	Microarray
Soares et al. 2013	2053*	FDR<1%	SILAC			
Wisniewski and Rakus, 2014	2200	FDR<1%	FASP			
Raghavan et al. 2011				Genes: 4161, 133 sRNA	%region mapped ≥50%	RNA-seq

\*The criteria that Soares et al. use for a protein being observed is that it appear in at least 1 of 2 biological repeats. We use a criteria that it appear in 1 of 3 biological repeats.

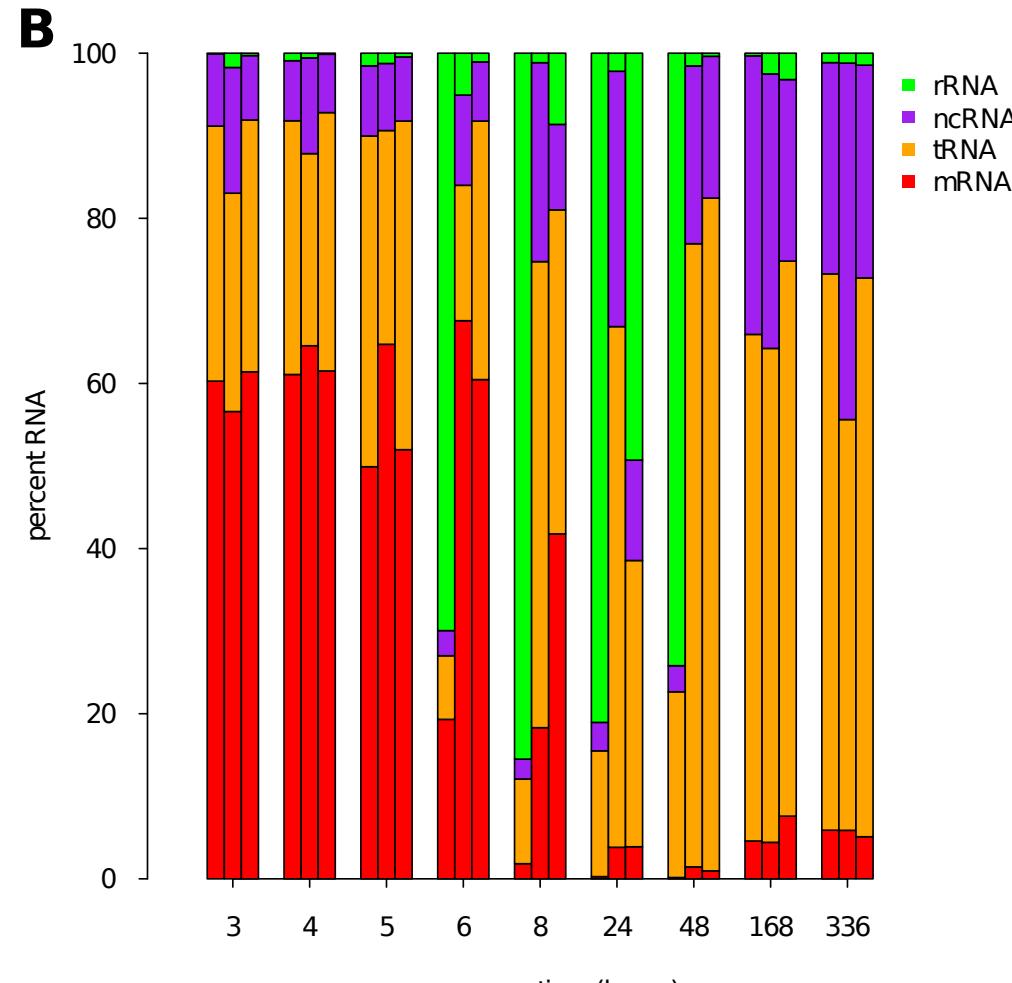
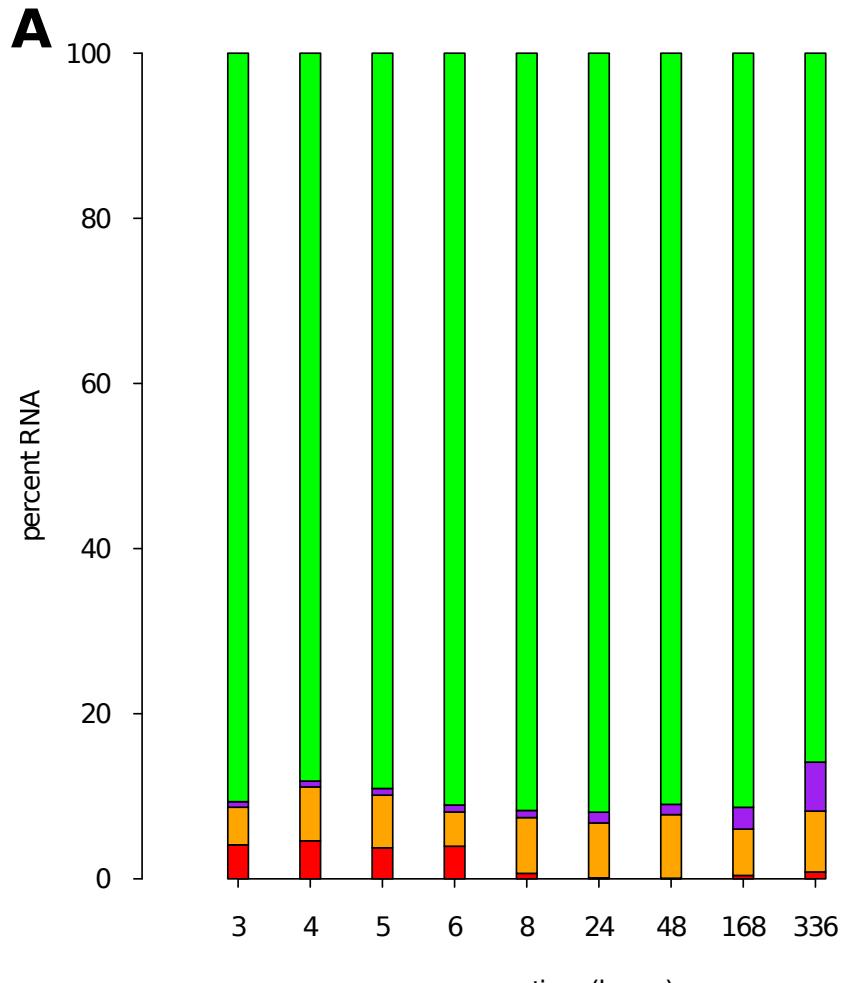
# Figure S1



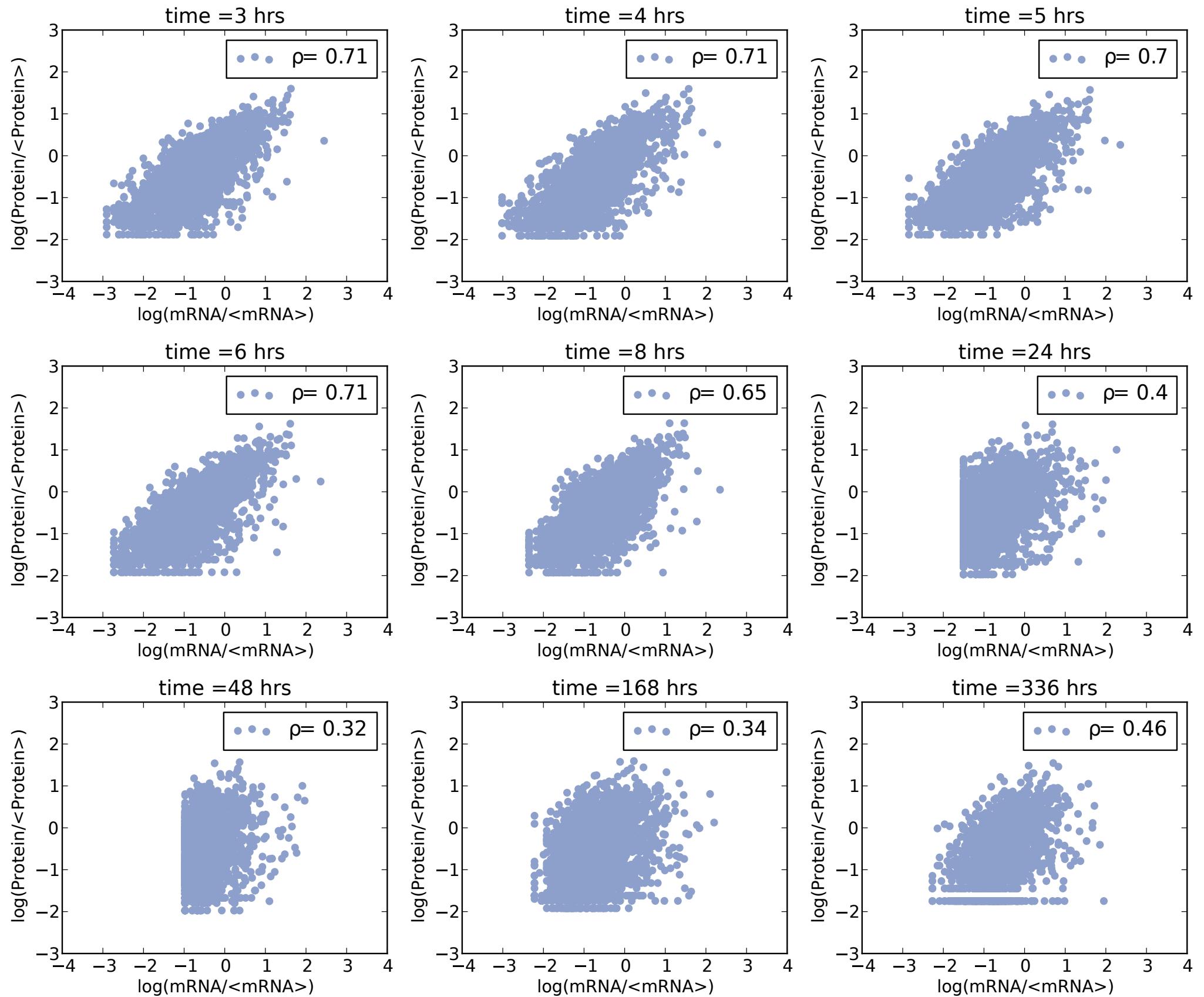
# Figure S2



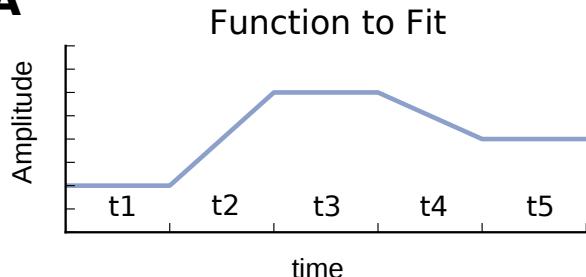
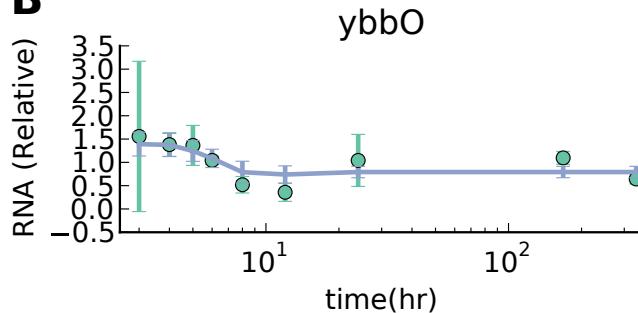
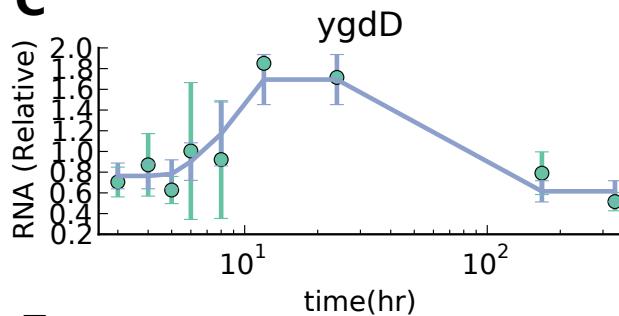
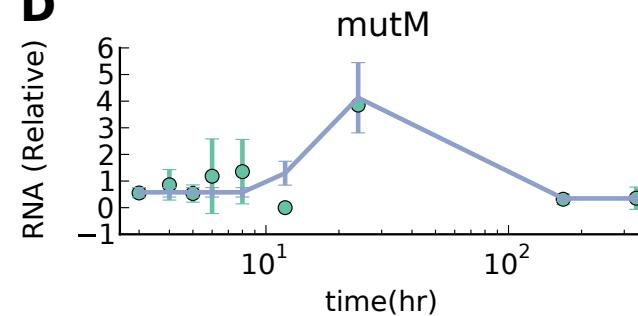
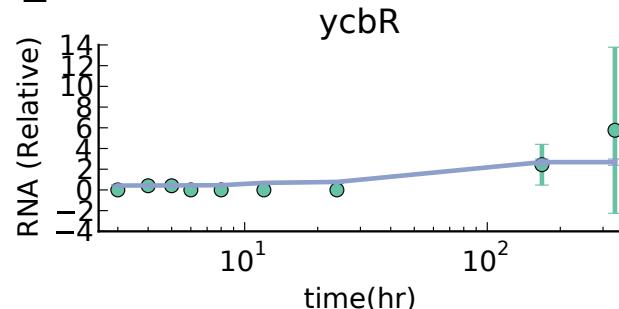
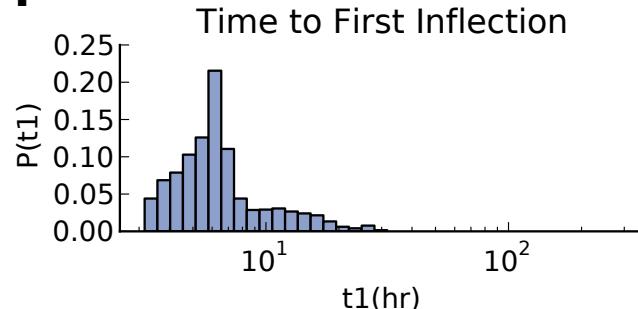
# Figure S3



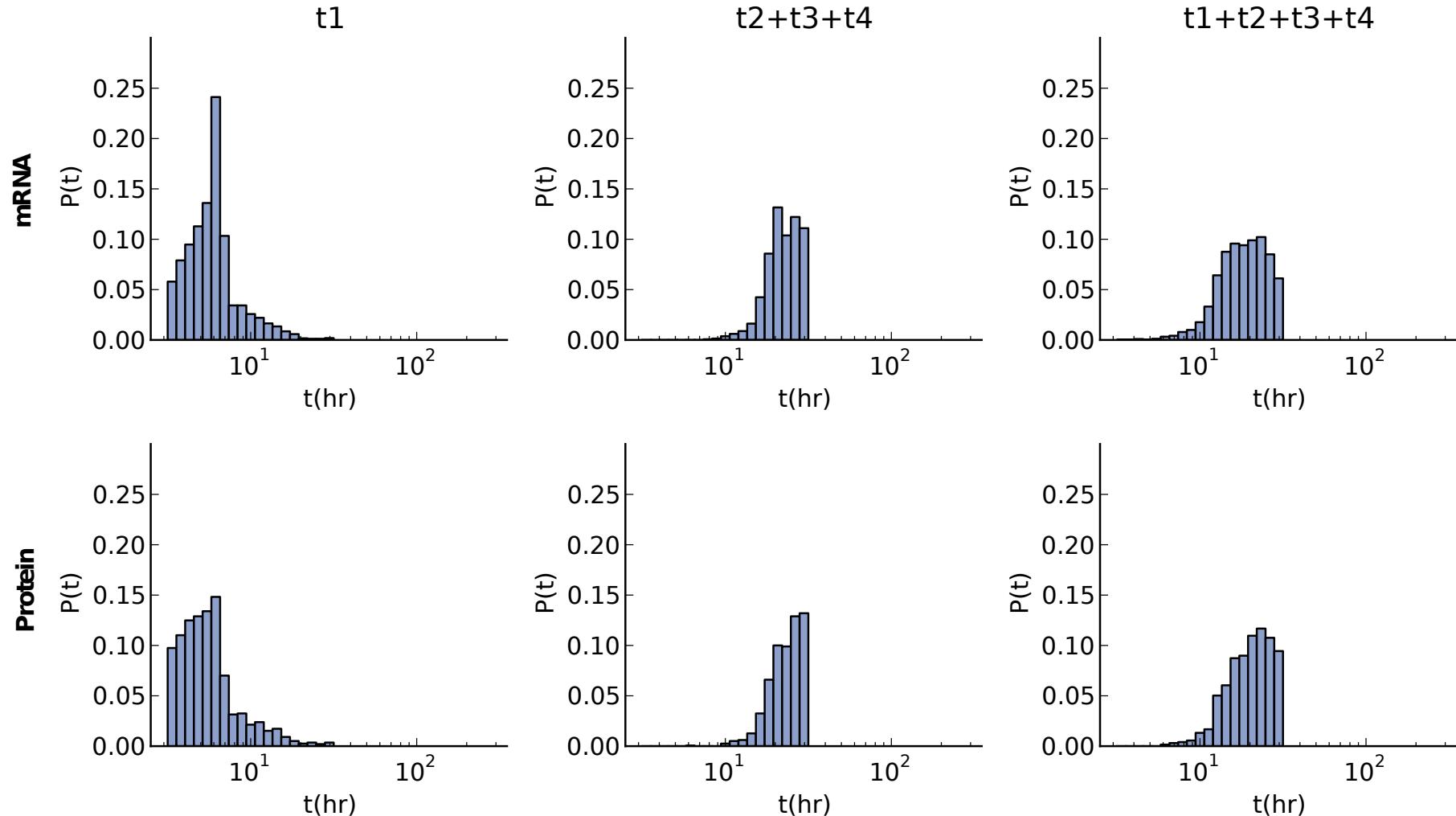
# Figure S4



# Figure S5

**A****B****C****D****E****F**

# Figure S6



# Figure S7

